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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant:	YAMAKAWA, Naomi	***Confirmation No.:***	9927
Serial No.	10/590,122	***Group Art Unit:***	1639
Filed:	August 18, 2006	***Examiner:***	STEELE, Amber D.
Docket No.	2352.016		
Title:	DNA ARRAY FOR ANALYZING DNA METHYLATION, METHOD OF PRODUCING THE SAME AND METHOD OF ANALYZING DNA METHYLATION		

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

RESPONSE TO RESTRICTION REQUIREMENT

Dear Sir:

This is in response to the Office Action mailed on January 14, 2009, in connection with the above-identified U.S. patent application. The one-month period for response expires on February 14, 2009. Accordingly, this response is timely filed.

Claims 1-13 were presented at the time of filing and are currently pending in the application. The Action of January 14, 2009 requires election under 35 U.S.C. 121 and 372 between four groups of claims:

Group I – claim(s) 1-6 and 12-13, drawn to a method of producing a DNA array;

Group II – claim(s) 7-9, drawn to a DNA array;

Group III – claim(s) 10, drawn to a method of analyzing a modification in a DNA; and

Group IV – claim(s) 11, drawn to a method of purifying dsDNA fragments.

Applicants hereby provisionally elect the claims of Group III (claim 10), drawn to a method of analyzing a modification in a DNA, with traverse as to Groups I and II.

According to the Action, the inventions do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features. According to the Action, the common technical feature is a library of DNA fragments having cohesive ends and modified bases. Furthermore, according to the Action, Barany et al. teach LDR and LCR reactions on arrays wherein the LDR and LCR nucleic acids and final products are modified.

Independent claim 10 of the present invention is directed to a method of analyzing a modification in a DNA to be assayed. The method comprises the steps of preparing a mixture of DNA fragments in which a modified base (as that term is known to those of skill in the art and also defined in the specification at page 11, ¶ [0028]), for example, methylated cytosine, or base (unmodified) is exposed; bringing the mixture of DNA fragments into contact with an antibody specific to the modified base or unmodified base and separating the fragments in the mixture into groups depending on whether or not immunocomplexes were formed between the fragments and base-specific antibodies. This method forms the foundation of a method of producing a DNA array as claimed in independent claim 1. Thus, the common technical feature is the method of preparing a mixture of DNA fragments in which a modified base or unmodified base is exposed by restriction enzymes, followed by separation of fragments into groups based on their ability to be bound by base-specific antibody.

The method of Barany *et al.* differs from the claimed invention in at least two respects: 1) the disclosed method seeks to detect nucleotide sequence differences, for example, substituted bases, base insertions, base deletions, but not base modifications, such as methylation; and 2) does so using oligonucleotide probes rather than base-specific antibodies. Thus, the method of Barany *et al.* does not disclose the common technical feature of the claimed invention.

In as much as the current claims do not lack a special technical feature common to all claims, withdrawal of the restriction is respectfully requested.

The Examiner is invited to contact Applicants' Attorney at the telephone number given below if any further questions arise in connection with this Application.

Respectfully submitted,

Kathy Smith Dias
Attorney for Applicants
Registration No.: 41,707

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Address for Correspondence:
HESLIN ROTHENBERG FARLEY & MESITI P.C.
5 Columbia Circle
Albany, New York 12203-5160
Telephone: (518) 452-5600
Facsimile: (518) 452-5579